

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/567,536
Source: IFUO
Date Processed by STIC: 1/15/07

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IFWO

RAW SEQUENCE LISTING

DATE: 01/05/2007

PATENT APPLICATION: US/10/567,536

TIME: 14:14:51

Input Set : N:\efs\01_05_07\10567536_efs\Seqlist.txt
 Output Set: N:\CRF4\01052007\J567536.raw

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4 <110> APPLICANT: HITCHMAN, Tim
5   ROBERTSON, Dan E.
6   HIRAIWA, Masao
7   PHILLIPS, Yoko
8   GRAY, Kevin
10 <120> TITLE OF INVENTION: LACCASES, NUCLEIC ACIDS ENCODING THEM AND METHODS
11   FOR MAKING AND USING THEM
13 <130> FILE REFERENCE: 564462012600
15 <140> CURRENT APPLICATION NUMBER: US 10/567,536
C--> 16 <141> CURRENT FILING DATE: 2006-02-07
18 <150> PRIOR APPLICATION NUMBER: PCT/US2004/025932
19 <151> PRIOR FILING DATE: 2004-08-11
21 <150> PRIOR APPLICATION NUMBER: US 60/494,472
22 <151> PRIOR FILING DATE: 2003-08-11
24 <160> NUMBER OF SEQ ID NOS: 26
26 <170> SOFTWARE: FastSEQ for Windows Version 4.0
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 1542
30 <212> TYPE: DNA
31 <213> ORGANISM: Unknown
33 <220> FEATURE:
34 <223> OTHER INFORMATION: Obtained from an environmental sample
36 <400> SEQUENCE: 1
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39 cgcgatctcc ctccaacccg cttgtggggc tataacgggtt tattccccgg tcccaccatt 180
40 aaggccaaaa gaaatgaaaa cgtttatgtg aaatggatga ataaccttcc ttcaagagcat 240
41 tttcttccga ttgatcacac cattcatcac agtgacagcc agcatgccga acccgagg 300
42 aaaaccgtcg ttcatttaca cggcgccgtc actccagatg acagcgacgg ttatctgag 360
43 gcctggtttt ctaaagactt tgaacaaaca ggcccttatt ttaaacgaga ggtttaccat 420
44 tatccaaatc agcagcgcgg agctatttt tggtatcacg atcatgctat ggcgctcacg 480
45 aggctgaatg tgtatgcgg gctcatcggt gcttataatca tccatgaacc aaaggaaaaa 540
46 cgccctgaagc tcccattcagg tgaatacgat gtgccgctt tgatcacgga ccgtacgatt 600
47 aatgaagatg gcttttatt ttatccgagc ggaccggaaa acccttcacc gtcactgcct 660
48 aatccgtcaa tcgttccagc ctttgcgg aatacaattc tcgtcaacgg gaaggcatgg 720
49 ccatacatgg aggtcgaacc gagaaaaatac cgcttcccg cgcatcaatgc ctctaatacg 780
50 agaacatata acctgtcact tgataatggg ggagaattta tccagatcggt ttctgacggc 840
51 ggactttgc cgcgctccgt caagctaaac tctttcagta tcgcgccagc tgagcgctt 900
52 gatatcctca ttgacttcgc cgcgttggaa ggacaatcga ttattttagc aaacagcgag 960
53 ggctgcggcg ggcgacgttaa tccggaaaca gacgcaaaaca tcgtcaatt cagagtac 1020
54 aaaccgttag cccaaaaaga cgaaagcaga aagccaaaat acctggcatc ttacccttca 1080
55 gtacggcagc aaagaataca aaacctccga acattgaagc tggcaggaac tcaagatcaa 1140
56 tacggcagac ccgttcttct tcttaacaac aaacgctggc acgtcctgt cactgaagca 1200

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57	ccgaaagccg	gttctaccga	aatatggtcg	atcatcaatc	cgacacgcgg	aacacatccc	1260										
58	atccatcttc	atttggtctc	cttccgtgt	ttggaccggc	gcccatttga	tacagcccg	1320										
59	tttgaagagc	gcggagaact	ggcctacacc	ggaccggccg	ttccgcccgc	accaagtgaa	1380										
60	aaaggctgga	aagacacggt	tcagtcacac	gccggtaag	tcctgagaat	cggcgtaaaca	1440										
61	ttcgggccc	atca	ctggcg	gtacgtatgg	cattgccaca	ttcttgagca	1500										
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74	1			5			10				15						
75	Lys	Pro	Val	Gln	Gln	Ser	Lys	Asp	Ser	Thr	Tyr	Tyr	Glu	Val	Thr	Met	
76				20			25				30						
77	Glu	Glu	Cys	Tyr	His	Gln	Leu	His	Arg	Asp	Leu	Pro	Pro	Thr	Arg	Leu	
78				35			40				45						
79	Trp	Gly	Tyr	Asn	Gly	Leu	Phe	Pro	Gly	Pro	Thr	Ile	Lys	Ala	Lys	Arg	
80				50			55				60						
81	Asn	Glu	Asn	Val	Tyr	Val	Lys	Trp	Met	Asn	Asn	Leu	Pro	Ser	Glu	His	
82	65			65			70			75			80				
83	Phe	Leu	Pro	Ile	Asp	His	Thr	Ile	His	His	Ser	Asp	Ser	Gln	His	Ala	
84				85			85			90			95				
85	Glu	Pro	Glu	Val	Lys	Thr	Val	Val	His	Leu	His	Gly	Gly	Val	Thr	Pro	
86				100			100			105			110				
87	Asp	Asp	Ser	Asp	Gly	Tyr	Pro	Glu	Ala	Trp	Phe	Ser	Lys	Asp	Phe	Glu	
88				115			115			120			125				
89	Gln	Thr	Gly	Pro	Tyr	Phe	Lys	Arg	Glu	Val	Tyr	His	Tyr	Pro	Asn	Gln	
90				130			130			135			140				
91	Gln	Arg	Gly	Ala	Ile	Leu	Trp	Tyr	His	Asp	His	Ala	Met	Ala	Leu	Thr	
92	145			145			150			155			160				
93	Arg	Leu	Asn	Val	Tyr	Ala	Gly	Leu	Ile	Gly	Ala	Tyr	Ile	Ile	His	Glu	
94				165			165			170			175				
95	Pro	Lys	Glu	Lys	Arg	Leu	Lys	Leu	Pro	Ser	Gly	Glu	Tyr	Asp	Val	Pro	
96				180			180			185			190				
97	Leu	Leu	Ile	Thr	Asp	Arg	Thr	Ile	Asn	Glu	Asp	Gly	Ser	Leu	Phe	Tyr	
98				195			195			200			205				
99	Pro	Ser	Gly	Pro	Glu	Asn	Pro	Ser	Pro	Ser	Leu	Pro	Asn	Pro	Ser	Ile	
100				210			210			215			220				
101	Val	Pro	Ala	Phe	Cys	Gly	Asp	Thr	Ile	Leu	Asn	Gly	Lys	Ala	Trp		
102	225			225			225			230			235			240	
103	Pro	Tyr	Met	Glu	Val	Glu	Pro	Arg	Lys	Tyr	Arg	Phe	Arg	Val	Ile	Asn	
104				245			245			250			255				
105	Ala	Ser	Asn	Thr	Arg	Thr	Tyr	Asn	Leu	Ser	Leu	Asp	Asn	Gly	Gly	Glu	
106				260			260			265			270				
107	Phe	Ile	Gln	Ile	Gly	Ser	Asp	Gly	Gly	Leu	Leu	Pro	Arg	Ser	Val	Lys	
108				275			275			280			285				

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109 Leu Asn Ser Phe Ser Ile Ala Pro Ala Glu Arg Phe Asp Ile Leu Ile
110 290 295 300
111 Asp Phe Ala Ala Phe Glu Gly Gln Ser Ile Ile Leu Ala Asn Ser Glu
112 305 310 315 320
113 Gly Cys Gly Gly Asp Val Asn Pro Glu Thr Asp Ala Asn Ile Met Gln
114 325 330 335
115 Phe Arg Val Thr Lys Pro Leu Ala Gln Lys Asp Glu Ser Arg Lys Pro
116 340 345 350
117 Lys Tyr Leu Ala Ser Tyr Pro Ser Val Arg His Glu Arg Ile Gln Asn
118 355 360 365
119 Leu Arg Thr Leu Lys Leu Ala Gly Thr Gln Asp Gln Tyr Gly Arg Pro
120 370 375 380
121 Val Leu Leu Leu Asn Asn Lys Arg Trp His Asp Pro Val Thr Glu Ala
122 385 390 395 400
123 Pro Lys Ala Gly Ser Thr Glu Ile Trp Ser Ile Ile Asn Pro Thr Arg
124 405 410 415
125 Gly Thr His Pro Ile His Leu His Leu Val Ser Phe Arg Val Leu Asp
126 420 425 430
127 Arg Arg Pro Phe Asp Thr Ala Arg Phe Glu Glu Arg Gly Glu Leu Ala
128 435 440 445
129 Tyr Thr Gly Pro Ala Val Pro Pro Pro Ser Glu Lys Gly Trp Lys
130 450 455 460
131 Asp Thr Val Gln Ser His Ala Gly Glu Val Leu Arg Ile Ala Val Thr
132 465 470 475 480
133 Phe Gly Pro Tyr Thr Gly Arg Tyr Val Trp His Cys His Ile Leu Glu
134 485 490 495
135 His Glu Asp Tyr Asp Met Met Arg Pro Met Asp Val Ile Asp Pro His
136 500 505 510

137 Lys Ser

140 <210> SEQ ID NO: 3
141 <211> LENGTH: 1626
142 <212> TYPE: DNA
143 <213> ORGANISM: Unknown

145 <220> FEATURE:

146 <223> OTHER INFORMATION: Obtained from an environmental sample

148 <400> SEQUENCE: 3

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150 cttgtcgccg	ctggcgctc	cggcttcgt	acgtcgccg	aggtccggc	gcaaccccgt	120
151 gctgcgaatc	cgcagttcat	cccgacactc	gagatccagt	tgaacgctcg	ggaagatcat	180
152 gtgtcgatcc	tgcctggacc	actcactcgc	gtctggcggt	acgacggcaa	agtcgtgaag	240
153 ggcgatccgg	gcaacctggc	tttcctgtcg	aacggattt	tacccgtgg	gcmcgtcg	300
154 cgcggacaga	aagtgcgtat	cgatttcgtc	aaccagttag	ctgagccgac	catcatccac	360
155 tggcatggcc	tgtacgtgcc	agcagcaatg	gatggacatc	cgcgaatgc	ggtttcgacc	420
156 ggcgagcact	acgtgtacga	gttcgagatc	gccaaccagg	cagggacgta	ctggttcat	480
157 ggcgcaccccg	acggtcgtac	gggagcaca	atttacttcg	gactggcg	ggtattgatc	540
158 gtcgacgatg	aggaggcg	cgccgggtt	cccgaaagg	cgtacgatgt	accgctcg	600
159 attcaggacc	gcacgttcga	cgatcggaa	cagttcacgt	atctcgccga	aggcaatgag	660
160 gggatgtgg	gcccgtat	ggcaacggc	ggcatgtgg	gacgcgggg	catgtatggc	720
161 ggaggcggca	tggggcagat	gatggcg	atgatgggtt	tcctcg	ccggattctc	780

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162	gtcaacggca	agccccactt	cgtgctgccg	gtggctgccc	gtgcctatcg	ccttcgtttg	840										
163	ctgaatgggt	cgaacacgcg	tatctacaag	cttgcgtgga	gcccggac	accacctacg	900										
164	gtaatcggt	cgacggcgg	actgctggaa	cggccgggtga	cgcgccaata	cgtcacgctg	960										
165	gcccggccg	agcgcgtgga	cgtctgggt	gatttcagtc	gatggccgt	cggcacgaag	1020										
166	ctgacgctgc	agagtctggc	gttcgacggc	gtcctggcca	tgggcggcat	gatcggcaac	1080										
167	acctcgttac	cgagcggcgc	gtcggtcccg	gtcctgaagg	tcggcgtcga	ccagcgtgctg	1140										
168	aacacaaaaga	tggaactgcc	ggcgcggctc	gcatcgctgc	caccgggtcg	ccctcaggac	1200										
169	gccgtcaatg	cgcacaatcc	gaagggtgttc	aacatcacga	tgggcatgtat	ggtctggggc	1260										
170	gtcaacgggc	gtcgcttcga	aatgaacggg	gtggcgaaaa	cggagaccgt	gagacgcaac	1320										
171	agcacggaaa	tctggagtt	ccgcaacgag	gaatcgatga	tgctgatggc	ccattcgatg	1380										
172	cacgttcacg	ggctgcagtt	ccgtgtgtctg	gagcgttaccg	tccagccgga	tttcagagcc	1440										
173	ggttaccgca	cgctggcagc	gggactgggt	gatgatggct	ggaaagacac	cgtgttattg	1500										
174	atgcccgggt	agcgtatccg	cctgctgtc	cggttcgcga	gctacacggg	cctgtttctt	1560										
175	taccattgtc	acatgctgga	gcacgaagat	tccggattga	tgcgttaacta	cctgatccag	1620										
176	acgtaa						1626										
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181	<213>	ORGANISM:	Unknown														
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193	Thr	Met	Ser	Cys	Leu	Val	Ala	Ala	Gly	Ala	Ser	Gly	Leu	Leu	Thr	Leu	
194					20				25				30				
195	Arg	Glu	Val	Arg	Ala	Gln	Pro	Arg	Ala	Ala	Asn	Pro	Gln	Phe	Ile	Pro	
196					35				40				45				
197	Asp	Leu	Glu	Ile	Gln	Leu	Asn	Ala	Arg	Glu	Asp	His	Val	Ser	Ile	Leu	
198					50				55				60				
199	Pro	Gly	Pro	Leu	Thr	Arg	Val	Trp	Arg	Tyr	Asp	Gly	Lys	Val	Val	Lys	
200					65				70				75			80	
201	Gly	Asp	Pro	Gly	Asn	Leu	Ala	Phe	Leu	Ser	Asn	Gly	Tyr	Leu	Pro	Val	
202						85				90			95				
203	Val	Arg	Val	Arg	Arg	Gly	Gln	Lys	Val	Arg	Ile	Asp	Phe	Val	Asn	Gln	
204						100				105			110				
205	Leu	Ala	Glu	Pro	Thr	Ile	Ile	His	Trp	His	Gly	Leu	Tyr	Val	Pro	Ala	
206						115				120			125				
207	Ala	Met	Asp	Gly	His	Pro	Arg	Asn	Ala	Val	Ser	Thr	Gly	Glu	His	Tyr	
208						130				135			140				
209	Val	Tyr	Glu	Phe	Glu	Ile	Ala	Asn	Gln	Ala	Gly	Thr	Tyr	Trp	Phe	His	
210						145				150			155			160	
211	Ala	His	Pro	Asp	Gly	Arg	Thr	Gly	Ala	Gln	Ile	Tyr	Phe	Gly	Leu	Ala	
212							165				170			175			
213	Gly	Val	Leu	Ile	Val	Asp	Asp	Glu	Glu	Ala	Ala	Gly	Leu	Pro	Glu		
214							180				185			190			

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215 Gly Pro Tyr Asp Val Pro Leu Val Ile Gln Asp Arg Thr Phe Asp Asp
 216 195 200 205
 217 Arg Asn Gln Phe Thr Tyr Leu Ala Glu Gly Asn Glu Gly Met Met Gly
 218 210 215 220
 219 Gly Met Met Gly Asn Gly Gly Met Met Gly Arg Gly Gly Met Met Gly
 220 225 230 235 240
 221 Gly Gly Met Gly Gln Met Met Ala Arg Met Met Gly Phe Leu Gly
 222 245 250 255
 223 Asp Arg Ile Leu Val Asn Gly Lys Pro Asp Phe Val Leu Pro Val Ala
 224 260 265 270
 225 Ala Arg Ala Tyr Arg Leu Arg Leu Leu Asn Gly Ser Asn Thr Arg Ile
 226 275 280 285
 227 Tyr Lys Leu Ala Trp Ser Asp Arg Thr Pro Leu Thr Val Ile Gly Thr
 228 290 295 300
 229 Asp Gly Gly Leu Leu Glu Arg Pro Val Thr Arg Gln Tyr Val Thr Leu
 230 305 310 315 320
 231 Ala Pro Ala Glu Arg Val Asp Val Trp Val Asp Phe Ser Arg Trp Pro
 232 325 330 335
 233 Val Gly Thr Lys Leu Thr Leu Gln Ser Leu Ala Phe Asp Gly Val Leu
 234 340 345 350
 235 Ala Met Gly Gly Met Ile Gly Asn Thr Ser Leu Pro Ser Gly Ala Ser
 236 355 360 365
 237 Phe Pro Val Leu Lys Val Gly Val Asp Gln Arg Ala Asn Thr Lys Met
 238 370 375 380
 239 Glu Leu Pro Ala Arg Leu Ala Ser Leu Pro Pro Val Arg Pro Gln Asp
 240 385 390 395 400
 241 Ala Val Asn Ala His Asn Pro Lys Val Phe Asn Ile Thr Met Gly Met
 242 405 410 415
 243 Met Val Trp Gly Val Asn Gly Arg Arg Phe Glu Met Asn Gly Val Ala
 244 420 425 430
 245 Lys Thr Glu Thr Val Arg Arg Asn Ser Thr Glu Ile Trp Glu Phe Arg
 246 435 440 445
 247 Asn Glu Glu Ser Met Met Leu Met Ala His Ser Met His Val His Gly
 248 450 455 460
 249 Leu Gln Phe Arg Val Leu Glu Arg Thr Val Gln Pro Asp Phe Arg Ala
 250 465 470 475 480
 251 Gly Tyr Arg Thr Leu Ala Ala Gly Leu Val Asp Asp Gly Trp Lys Asp
 252 485 490 495
 253 Thr Val Leu Leu Met Pro Gly Glu Arg Ile Arg Leu Leu Leu Arg Phe
 254 500 505 510
 255 Ala Ser Tyr Thr Gly Leu Phe Leu Tyr His Cys His Met Leu Glu His
 256 515 520 525
 257 Glu Asp Ser Gly Leu Met Arg Asn Tyr Leu Ile Gln Thr
 258 530 535 540
 260 <210> SEQ ID NO: 5
 261 <211> LENGTH: 1584
 262 <212> TYPE: DNA
 263 <213> ORGANISM: Bacteria
 265 <400> SEQUENCE: 5

VERIFICATION SUMMARY

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L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date